



45

# SEQUENCE LISTING

<110> WEI, Ming-Hui et al

<120> ISOLATED HUMAN PHOSPHATASE PROTEINS,  
NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,  
AND USES THEREOF

<130> CL000964-CIP

<140> 09/761,640

<141> 2001-01-18

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2704

<212> DNA

<213> Human

<400> 1

```
cgctccttccct ggtcctgcgg gtccaggact gtccgcgggg ttgaggaag gggccgtgcc 60
cgggtgccagc ccagggtgctc gcggcctggc tccatggccc tggtcacagt gagccgttcg 120
ccccggggca gcggcgccctc cagccccgtg gggccctggg accaggcggg ccagcgaagg 180
agtcgactcc agcgaaggca gagctttgct gtgctccgtg gggctgtcct gggactgcag 240
gatggagggg acaatgatga tgcagcagag gccagttctg agccaacaga gaaggccccg 300
agtgaggagg agctccacgg ggaccagaca gacttcgggc aaggatcca gagtccccag 360
aagcaggagg agcagaggca gcacctgcac ctcatggtac agctgctgag gccgcaggat 420
gacatccgcc tggcagccca gctggaggca cccggcctc cccggctccg ctacctgctg 480
gtagtttcta cagcagaagg agaaggctct agccaggatg agacggctct cctgggcgtg 540
gatttccctg acagcagctc cccagctgc accctgggcc tggctctgcc cctctggagt 600
gacacccagg tgtacttaga tggagacggg ggcttcagcg tgacgtctgg tgggcaaagc 660
cggatcttca agcccatctc catccagacc atgtgggcca cactccaggt attgcaccaa 720
gcatgtgagg cagctctagg cagcggcctt gtaccgggtg gcagtgcctt cacctgggcc 780
agccactacc aggagagact gaactccgaa cagagctgcc tcaatgagtg gacggctatg 840
gccgacctgg agtctctgct gcctcccagc gccgagcctg gcgggtcctc agaacaggag 900
cagatggagc aggcgatccg tgctgagctg tggaaagtgt tggatgtcag tgacctggag 960
agtgtcactt ccaaagagat ccgccaggct ctggagctgc gcctggggct cccctccag 1020
cagtaccgtg acttcatcga caaccagatg ctgctgctgg tggcacagcg ggaccgagcc 1080
tccgcctctt tccccacct ctacctgggc tcagagtggg acgcagcaa cctggaggag 1140
ctgcagagga acagggtcac ccacatcttg aacatggccc gggagattga caacttctac 1200
cctgagcgct tcacctacca caatgtgcgc ctctgggatg aggagtcggc ccagctgctg 1260
ccgcactgga aggagacgca ccgcttcatt gaggctgcaa gagcacagg caccacgtg 1320
ctggtccact gcaagatggg cgtcagccgc tcagcggcca cagtgtggc ctatgccatg 1380
aagcagtacg aatgcagcct ggagcaggcc ctgcgccacg tgcaggagct ccggcccatc 1440
gcccgcacca accctggctt cctgcgccag ctgcagatct accaggcat cctgacggcc 1500
agaacctgag ggtggtgggg aggagaaggt tgtaggcatg gaagagagcc aggcagcccc 1560
gaaagaagag cctggggccac ggccacgtat aaacctccga ggggtcatga ggtccatcag 1620
tcttctggag ccctccttgg agctggagag cacctcagag accagtgaca tgccagaggt 1680
cttctcttcc cagcagctct cacaatgaaga gcctctgcag cccttcccac agcttgcaag 1740
gaccaaggga ggccagcagg tggacagggg gcctcagcct gccctgaagt cccgccagtc 1800
agtggttacc ctccagggca gtgccgtggt ggccaaccgg acccaggcct tccaggagca 1860
ggagcagggg caggggcagg ggcagggaga gccctgcatt tcctctacgc ccaggttccg 1920
gaaggtggtg agacaggcca gcgtgcatga cagtggagag gagggcgagg cctgagccct 1980
```

cacacatgcc	cacgctcccc	tgacactgaa	gaggatccac	aactccttgg	agaaacaccc	2040
tcacgtctgt	tgccgcacac	attcctctca	gctccgcccc	ataccctgtca	ctacagcctc	2100
acctcccacc	cctgtcacta	cggcctcacc	tcccaccctt	gtcactacag	cctcacctcc	2160
tacagcctta	agtcccaggc	ccatgtctgc	ctgtccaagg	gctcaagact	ttctaactgg	2220
gatgtggtag	agggactgaa	ggtacctttg	ggggcaacag	caccctagtt	tcattctcaa	2280
ctctagccct	gcacactcac	ctgtggcacg	gaatgaaaac	agagcttccc	gtgcaaaaag	2340
ggtcacgcct	cccacccccg	ccccctccct	gcacctcctg	tcctctccca	gttcattcct	2400
ggaaccagcc	aggccaggca	accagtggcc	cccaaaggca	ggcaggatcc	tcaggcccca	2460
gccgcgggag	gctggaagg	ctggcagatc	gcttccctca	tccacctcca	ccggtccagg	2520
tctttgctgc	tgtccccaga	cctcctgtga	caccacgcca	gatcacagg	caccaggcca	2580
gagatagtct	tctttttgtc	ctttctggcc	tctggctagt	cagtttttca	tagccttaca	2640
gtatctggct	ttgtactgag	aaataaaaaca	cattttcata	aaaaaaaaaa	aaaaaaaaaa	2700
aaaa						2704

<210> 2

<211> 2852

<212> DNA

<213> Human

<400> 2

tggttgaggg	aaggggccgt	gcccgggtgcc	agcccagggtg	ctcgcggcct	ggctccatgg	60
ccctggtcac	agtgagccgt	tcgcccccg	gcagcggcgc	ctccacgccc	gtggggccct	120
gggaccaggc	ggtccagcga	aggagtgcac	tccagcgaag	gcagagcttt	gcggtgctcc	180
gtggggctgt	cctgggactg	caggatggag	gggacaatga	tgatgcagca	gaggccagtt	240
ctgagccaac	agagaaggcc	ccgagtgagg	aggagctcca	cggggaccag	acagacttcg	300
ggcaaggatc	ccagagtccc	cagaagcagg	aggagcagag	gcagcacctg	cacctcatgg	360
tacagctgct	gaggccgcag	gatgacatcc	gcctggcagc	ccagctggag	gcaccccggc	420
ctccccggct	ccgtacctg	ctggtagttt	ctacacgaga	aggagaagg	ctgagccagg	480
atgagacggt	cctcctgggc	gtggatttcc	ctgacagcag	ctccccagc	tgcaccttga	540
gcctggctct	gcccctctgg	agtgcacccc	aggtgtactt	agatggagac	gggggcttca	600
gcgtgacgtc	tggtgggcaa	agccggatct	tcaagcccat	ctccatccag	accatgtggg	660
ccacactcca	ggtattgcac	caagcatgtg	aggcagctct	aggcagcggc	cttgtaccgg	720
gtggcagtgc	cctcacctgg	gccagccact	accaggagag	actgaactcc	gaacagagct	780
gcctcaatga	gtggacggct	atggccgacc	tggagtctct	gcggcctccc	agcgcgcagc	840
ctggcgggtc	ctcagaacag	gagcagatgg	agcaggcgat	ccgtgctgag	ctgtggaaag	900
tgttggtatg	cagtgaacctg	gagagtgtca	cttccaaaga	gatccgccag	gctctggagc	960
tgcgccctgg	gctccccctc	cagcagtacc	gtgacttcat	cgacaaccag	atgctgctgc	1020
tggtggcaca	gcgggaccga	gcctcccgcg	tcttccccca	cctctacctg	ggctcagagt	1080
ggaacgcagc	aaacctggag	gagctgcaga	ggaacagggt	caccacatc	ttgaacatgg	1140
cccgggagat	tgacaacttc	taccctgagc	gcttcacctt	ccacaatgtg	cgcctctggg	1200
atgaggagtc	ggcccagctg	ctgccgcact	ggaaggagac	gcaccgcttc	attgaggctg	1260
caagagcaca	gggcacccac	gtgctggtcc	actgcaagat	ggcgctcagc	cgctcagcgg	1320
ccacagtgtc	ggcctatgcc	atgaagcagt	acgaatgcag	cctggagcag	gccctgcgcc	1380
acgtgcagga	gctccggccc	atcgcccgc	ccaacctgtg	cttctgcgc	cagctgcaga	1440
tctaccagg	catcctgacg	gccagccgcc	agagccatgt	ctgggagcag	aaagtgggtg	1500
gggtctcccc	agaggagcac	ccagcccctg	aagtctctac	accattccca	cttcttcgc	1560
cagaacctga	gggtgggtgg	gaggagaagg	ttgtaggcat	ggaagagagc	caggcagccc	1620
cgaagaaga	gcctgggcca	cggccacgta	taaacctccg	aggggtcatg	aggtccatca	1680
gtcttctgga	gccctccttg	gagctggaga	gcacctcaga	gaccagtgtg	atgccagagg	1740
tcttctcttc	ccacgagtct	tcacatgaag	agcctctgca	gcccttccca	cagcttgcaa	1800
ggaccaagg	aggccagcag	gtggacagg	ggcctcagcc	tgccctgaag	tcccgcagct	1860
cagtggttac	cctccagggc	agtgccgtgg	tggccaaccg	gacccaggcc	ttccaggagc	1920
aggagcagg	gcaggggcag	gggcagggag	agccctgcat	ttcctctacg	cccagggttc	1980
ggaaggtggt	gagacaggcc	agcgtgcatg	acagtggaga	ggagggcgag	gcctgagccc	2040
tcacacatgc	ccacgtccc	ctgacactga	agaggatcca	caactccttg	gagaaacacc	2100
ctcacgtctg	ttgccgcaca	cattcctctc	agctccgccc	cataccctgc	actacagcct	2160
cacctccac	ccctgtcact	acggcctcac	ctcccacccc	tgtcactaca	gcctcacctc	2220

ctacagcctt	aagtcccagg	cccatgtctg	cctgtccaag	ggctcaagac	tttctaactg	2280
ggatgtggta	gagggactga	aggtaccttt	gggggcaaca	gcaccctagt	ttcatttctca	2340
actctagccc	tgcacactca	cctgtggcac	ggaatgaaaa	cagagcttcc	cgtgcaaaaa	2400
gggtcacgcc	tcccaccccc	gccccctccc	tgcacctcct	gtcctctccc	agttcattcc	2460
tggaaccagc	caggccaggc	aaccagtggc	ccccaaaggc	aggcaggatc	ctcaggccccc	2520
agccgcggga	ggctggaagg	gctggcagat	cgcttccctc	atccacctcc	accggtccag	2580
gtctttgctg	ctgtccccag	acctcctgtg	acaccacgcc	agatcacagg	gcaccaggcc	2640
agagatagtc	ttctttttgt	cctttctggc	ctctggctag	tcagtttttc	atagccttac	2700
agtatctggc	tttgtactga	gaaataaaac	acattttcat	aaaaaaaaaa	aaaaaaaaaa	2760
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	2820
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aa			2852

<210> 3

<211> 2540

<212> DNA

<213> Human

<400> 3

cctggtcctg	cgggtccagg	actgtcccgc	ggggttgagg	gaaggggccc	tgcccgggtgc	60
cagcccagggt	gctcgcgccc	tggctccatg	gccctgggtca	cagtgaagccg	ttcgcccccg	120
ggcagcggcg	cctccacgcc	cgtggggccc	tgggaccagg	cgggtccagcg	aaggagtcga	180
ctccagcgaa	ggcagagctt	tgcggtgctc	cgtggggctg	tcctgggact	gcaggatgga	240
ggggacaatg	atgatgcagc	agaggccagt	tctgagccaa	cagagaaggc	cccagagtga	300
gaggagctcc	acggggacca	gacagacttc	gggcaaggat	cccagagtcc	ccagaagcag	360
gaggagcaga	ggcagcacct	gcacctcatg	gtacagctgc	tgaggccgca	ggatgacatc	420
cgcttggcag	cccagctgga	ggcaccgccg	cctccccggc	tcgctacct	gctggtagtt	480
tctacacgag	aaggagaagg	tctgagccag	gatgagacgg	tcctcctggg	cgtggatttc	540
cctgacagca	gctccccag	ctgcacctg	ggcctgggtc	tgccccctctg	gagtgaacc	600
caggtgtact	tagatggaga	cgggggcttc	agcgtgacgt	ctggtgggca	aagccggatc	660
ttcaagccca	tctccatcca	gaccatgtgg	tcctcagaac	aggagcagat	ggagcaggcg	720
atccgtgtcg	agctgtggaa	agtgttggat	gtcagtgacc	tggagagtgt	cacttccaaa	780
gagatccgcc	aggctctgga	gctgcgcctg	gggtccccc	tccagcagta	ccgtgacttc	840
atcgacaacc	agatgctgct	gctggtggca	cagcgggacc	gagcctcccg	catcttcccc	900
cacctctacc	tgggctcaga	gtggaacgca	gcaaacctgg	aggagctgca	gaggaacagg	960
gtcaccacaca	tcttgaacat	ggcccgggag	attgacaact	tctaccctga	gcgcttcacc	1020
taccacaatg	tgcgcctctg	ggatgaggag	tcggcccagc	tgctgccgca	ctggaaggag	1080
acgcaccgct	tcattgaggc	tgcaagagca	cagggcaccc	acgtgctggt	ccactgcaag	1140
atgggctgca	gccgctcagc	ggccacagtg	ctggcctatg	ccatgaagca	gtacgaatgc	1200
agcctggagc	aggccctgcg	ccacgtgcag	gagctccggc	ccatcgcccc	ccccaaccct	1260
ggcttcctgc	gccagctgca	gatctaccag	ggcatcctga	cggccagaac	ctgagggtgg	1320
tggggaggag	aaggttgtag	gcatggaaga	gagccaggca	gccccgaaa	aagagcctgg	1380
ggccacgggg	cacgtataaa	cctccgaggg	gtcatgaggt	ccatcagtct	tctggagccc	1440
tccttgggag	ctggagagca	cctcagtaga	ccagtacat	gccagaggtc	ttctcttccc	1500
acgagtcttc	acatgaagag	cctctgcagc	ccttcccaca	gcttgcaagg	accaaggagg	1560
gccagcagggt	ggacaggggg	cctcagcctg	ccctgaagtc	ccgccagtca	gtggttacc	1620
tccagggcag	tgccgtggtg	gccaaccgga	ccaggcctt	ccaggagcag	gagcaggggc	1680
aggggcaggg	gcagggagag	ccctgcattt	cctctacgcc	caggttccgg	aaggtggtga	1740
gacaggccag	cgtgcatgac	agtggagagg	agggcgaggc	ctgagccctc	acacatgcc	1800
acgtccccc	gacactgaag	aggatccaca	actccttggg	gaaacaccct	cacgtctgtt	1860
gccgcacaca	ttcctctcag	ctccgcccc	taccgctcac	tacagcctca	cctcccaccc	1920
ctgtcactac	ggcctcacct	cccacccttg	tcactacagc	ctcacctcct	acagccttaa	1980
gtcccaggcc	catgtctgcc	tgtccaaggg	ctcaagactt	tctaactggg	atgtggtaga	2040
gggactgaag	gtacctttgg	gggcaacagc	accctagttt	cattctcaac	tctagccctg	2100
cacactcacc	tgtggcacgg	aatgaaaaca	gagcttcccg	tgcaaaaagg	gtcacgcctc	2160
ccacccccgc	cccctccctg	cacctcctgt	cctctcccag	ttcattcctg	gaaccagcca	2220
ggccaggcaa	ccagtggccc	ccaaaggcag	gcaggatcct	caggcccccag	ccgcgggagg	2280
ctggaagggc	tggcagatcg	cttccctcat	ccacctccac	cgggtccagg	ctttgctgct	2340

```

gtccccagac ctctgtgac accacgccag atcacagggc accaggccag agatagtctt 2400
ctttttgtcc tttctggcct ctggctagtc agtttttcat agccttacag tatctggctt 2460
tgtactgaga aataaaacac attttcatat ttgggttaaaa aaaaaaaaaa aaaaaaaaaa 2520
aaaaaaaaaa aaaaaaaaaa                                     2540

```

<210> 4  
 <211> 471  
 <212> PRT  
 <213> Human

<400> 4

```

Met Ala Leu Val Thr Val Ser Arg Ser Pro Pro Gly Ser Gly Ala Ser
1          5          10          15
Thr Pro Val Gly Pro Trp Asp Gln Ala Val Gln Arg Arg Ser Arg Leu
20          25          30
Gln Arg Arg Gln Ser Phe Ala Val Leu Arg Gly Ala Val Leu Gly Leu
35          40          45
Gln Asp Gly Gly Asp Asn Asp Asp Ala Ala Glu Ala Ser Ser Glu Pro
50          55          60
Thr Glu Lys Ala Pro Ser Glu Glu Glu Leu His Gly Asp Gln Thr Asp
65          70          75          80
Phe Gly Gln Gly Ser Gln Ser Pro Gln Lys Gln Glu Glu Gln Arg Gln
85          90          95
His Leu His Leu Met Val Gln Leu Leu Arg Pro Gln Asp Asp Ile Arg
100          105          110
Leu Ala Ala Gln Leu Glu Ala Pro Arg Pro Pro Arg Leu Arg Tyr Leu
115          120          125
Leu Val Val Ser Thr Arg Glu Gly Glu Gly Leu Ser Gln Asp Glu Thr
130          135          140
Val Leu Leu Gly Val Asp Phe Pro Asp Ser Ser Ser Pro Ser Cys Thr
145          150          155          160
Leu Gly Leu Val Leu Pro Leu Trp Ser Asp Thr Gln Val Tyr Leu Asp
165          170          175
Gly Asp Gly Gly Phe Ser Val Thr Ser Gly Gly Gln Ser Arg Ile Phe
180          185          190
Lys Pro Ile Ser Ile Gln Thr Met Trp Ala Thr Leu Gln Val Leu His
195          200          205
Gln Ala Cys Glu Ala Ala Leu Gly Ser Gly Leu Val Pro Gly Gly Ser
210          215          220
Ala Leu Thr Trp Ala Ser His Tyr Gln Glu Arg Leu Asn Ser Glu Gln
225          230          235          240
Ser Cys Leu Asn Glu Trp Thr Ala Met Ala Asp Leu Glu Ser Leu Arg
245          250          255
Pro Pro Ser Ala Glu Pro Gly Gly Ser Ser Glu Gln Glu Gln Met Glu
260          265          270
Gln Ala Ile Arg Ala Glu Leu Trp Lys Val Leu Asp Val Ser Asp Leu
275          280          285
Glu Ser Val Thr Ser Lys Glu Ile Arg Gln Ala Leu Glu Leu Arg Leu
290          295          300
Gly Leu Pro Leu Gln Gln Tyr Arg Asp Phe Ile Asp Asn Gln Met Leu
305          310          315          320
Leu Leu Val Ala Gln Arg Asp Arg Ala Ser Arg Ile Phe Pro His Leu
325          330          335
Tyr Leu Gly Ser Glu Trp Asn Ala Ala Asn Leu Glu Glu Leu Gln Arg
340          345          350
Asn Arg Val Thr His Ile Leu Asn Met Ala Arg Glu Ile Asp Asn Phe
355          360          365

```

Tyr	Pro	Glu	Arg	Phe	Thr	Tyr	His	Asn	Val	Arg	Leu	Trp	Asp	Glu	Glu
	370					375					380				
Ser	Ala	Gln	Leu	Leu	Pro	His	Trp	Lys	Glu	Thr	His	Arg	Phe	Ile	Glu
385					390					395					400
Ala	Ala	Arg	Ala	Gln	Gly	Thr	His	Val	Leu	Val	His	Cys	Lys	Met	Gly
				405					410					415	
Val	Ser	Arg	Ser	Ala	Ala	Thr	Val	Leu	Ala	Tyr	Ala	Met	Lys	Gln	Tyr
			420					425					430		
Glu	Cys	Ser	Leu	Glu	Gln	Ala	Leu	Arg	His	Val	Gln	Glu	Leu	Arg	Pro
	435						440					445			
Ile	Ala	Arg	Pro	Asn	Pro	Gly	Phe	Leu	Arg	Gln	Leu	Gln	Ile	Tyr	Gln
	450					455					460				
Gly	Ile	Leu	Thr	Ala	Arg	Thr									
465					470										

<210> 5  
 <211> 659  
 <212> PRT  
 <213> Human

<400> 5															
Met	Ala	Leu	Val	Thr	Val	Ser	Arg	Ser	Pro	Pro	Gly	Ser	Gly	Ala	Ser
1				5					10					15	
Thr	Pro	Val	Gly	Pro	Trp	Asp	Gln	Ala	Val	Gln	Arg	Arg	Ser	Arg	Leu
			20					25					30		
Gln	Arg	Arg	Gln	Ser	Phe	Ala	Val	Leu	Arg	Gly	Ala	Val	Leu	Gly	Leu
		35					40					45			
Gln	Asp	Gly	Gly	Asp	Asn	Asp	Ala	Ala	Glu	Ala	Ser	Ser	Glu	Pro	
	50				55				60						
Thr	Glu	Lys	Ala	Pro	Ser	Glu	Glu	Glu	Leu	His	Gly	Asp	Gln	Thr	Asp
65				70					75					80	
Phe	Gly	Gln	Gly	Ser	Gln	Ser	Pro	Gln	Lys	Gln	Glu	Glu	Gln	Arg	Gln
				85				90						95	
His	Leu	His	Leu	Met	Val	Gln	Leu	Leu	Arg	Pro	Gln	Asp	Asp	Ile	Arg
			100					105					110		
Leu	Ala	Ala	Gln	Leu	Glu	Ala	Pro	Arg	Pro	Pro	Arg	Leu	Arg	Tyr	Leu
		115					120					125			
Leu	Val	Val	Ser	Thr	Arg	Glu	Gly	Glu	Gly	Leu	Ser	Gln	Asp	Glu	Thr
	130					135					140				
Val	Leu	Leu	Gly	Val	Asp	Phe	Pro	Asp	Ser	Ser	Ser	Pro	Ser	Cys	Thr
145				150					155					160	
Leu	Gly	Leu	Val	Leu	Pro	Leu	Trp	Ser	Asp	Thr	Gln	Val	Tyr	Leu	Asp
				165				170						175	
Gly	Asp	Gly	Gly	Phe	Ser	Val	Thr	Ser	Gly	Gly	Gln	Ser	Arg	Ile	Phe
		180						185					190		
Lys	Pro	Ile	Ser	Ile	Gln	Thr	Met	Trp	Ala	Thr	Leu	Gln	Val	Leu	His
		195				200						205			
Gln	Ala	Cys	Glu	Ala	Ala	Leu	Gly	Ser	Gly	Leu	Val	Pro	Gly	Gly	Ser
	210					215					220				
Ala	Leu	Thr	Trp	Ala	Ser	His	Tyr	Gln	Glu	Arg	Leu	Asn	Ser	Glu	Gln
225				230					235					240	
Ser	Cys	Leu	Asn	Glu	Trp	Thr	Ala	Met	Ala	Asp	Leu	Glu	Ser	Leu	Arg
			245					250						255	
Pro	Pro	Ser	Ala	Glu	Pro	Gly	Gly	Ser	Ser	Glu	Gln	Glu	Gln	Met	Glu
			260					265					270		
Gln	Ala	Ile	Arg	Ala	Glu	Leu	Trp	Lys	Val	Leu	Asp	Val	Ser	Asp	Leu

275				280				285							
Glu	Ser	Val	Thr	Ser	Lys	Glu	Ile	Arg	Gln	Ala	Leu	Glu	Leu	Arg	Leu
290				295				300							
Gly	Leu	Pro	Leu	Gln	Gln	Tyr	Arg	Asp	Phe	Ile	Asp	Asn	Gln	Met	Leu
305					310					315					320
Leu	Leu	Val	Ala	Gln	Arg	Asp	Arg	Ala	Ser	Arg	Ile	Phe	Pro	His	Leu
				325					330					335	
Tyr	Leu	Gly	Ser	Glu	Trp	Asn	Ala	Ala	Asn	Leu	Glu	Glu	Leu	Gln	Arg
				340					345					350	
Asn	Arg	Val	Thr	His	Ile	Leu	Asn	Met	Ala	Arg	Glu	Ile	Asp	Asn	Phe
				355					360					365	
Tyr	Pro	Glu	Arg	Phe	Thr	Tyr	His	Asn	Val	Arg	Leu	Trp	Asp	Glu	Glu
370					375					380					
Ser	Ala	Gln	Leu	Leu	Pro	His	Trp	Lys	Glu	Thr	His	Arg	Phe	Ile	Glu
385					390					395					400
Ala	Ala	Arg	Ala	Gln	Gly	Thr	His	Val	Leu	Val	His	Cys	Lys	Met	Gly
				405					410					415	
Val	Ser	Arg	Ser	Ala	Ala	Thr	Val	Leu	Ala	Tyr	Ala	Met	Lys	Gln	Tyr
				420					425					430	
Glu	Cys	Ser	Leu	Glu	Gln	Ala	Leu	Arg	His	Val	Gln	Glu	Leu	Arg	Pro
				435					440					445	
Ile	Ala	Arg	Pro	Asn	Pro	Gly	Phe	Leu	Arg	Gln	Leu	Gln	Ile	Tyr	Gln
450					455					460					
Gly	Ile	Leu	Thr	Ala	Ser	Arg	Gln	Ser	His	Val	Trp	Glu	Gln	Lys	Val
465					470					475					480
Gly	Gly	Val	Ser	Pro	Glu	Glu	His	Pro	Ala	Pro	Glu	Val	Ser	Thr	Pro
				485					490					495	
Phe	Pro	Leu	Leu	Pro	Pro	Glu	Pro	Glu	Gly	Gly	Gly	Glu	Glu	Lys	Val
				500					505					510	
Val	Gly	Met	Glu	Glu	Ser	Gln	Ala	Ala	Pro	Lys	Glu	Glu	Pro	Gly	Pro
				515					520					525	
Arg	Pro	Arg	Ile	Asn	Leu	Arg	Gly	Val	Met	Arg	Ser	Ile	Ser	Leu	Leu
530					535					540					
Glu	Pro	Ser	Leu	Glu	Leu	Glu	Ser	Thr	Ser	Glu	Thr	Ser	Asp	Met	Pro
545					550					555					560
Glu	Val	Phe	Ser	Ser	His	Glu	Ser	Ser	His	Glu	Glu	Pro	Leu	Gln	Pro
				565					570					575	
Phe	Pro	Gln	Leu	Ala	Arg	Thr	Lys	Gly	Gly	Gln	Gln	Val	Asp	Arg	Gly
				580					585					590	
Pro	Gln	Pro	Ala	Leu	Lys	Ser	Arg	Gln	Ser	Val	Val	Thr	Leu	Gln	Gly
				595					600					605	
Ser	Ala	Val	Val	Ala	Asn	Arg	Thr	Gln	Ala	Phe	Gln	Glu	Gln	Glu	Gln
610					615					620					
Gly	Gln	Gly	Gln	Gly	Gln	Gly	Glu	Pro	Cys	Ile	Ser	Ser	Thr	Pro	Arg
625					630					635					640
Phe	Arg	Lys	Val	Val	Arg	Gln	Ala	Ser	Val	His	Asp	Ser	Gly	Glu	Glu
				645					650					655	
Gly	Glu	Ala													

<210> 6  
 <211> 408  
 <212> PRT  
 <213> Human

<400> 6



<213> Human

<400> 7

```
cgtccttcct ggtcctgagg gtccaggact gtccgcgggg ttgaggggaag gggccgtgcc 60
cgggtgccagc ccagggtgctc gcggcctggc tccatggccc tggtcacagt gagccgttcg 120
ccccggggca gcggcgccctc cagcggcgtg gggccctggg accaggcggg ccagcgaagg 180
agtcgactcc agcgaaggca gagctttgcg gtgctccgtg gggctgtcct gggactgcag 240
gatggagggg acaatgatga tgcagcagag gccagttctg agccaacaga gaaggccccg 300
agtgaggagg agctccacgg ggaccagaca gacttcgggc aaggatccca gagtccccag 360
aagcaggagg agcagaggca gcacctgcac ctcatggtag agctgctgag gccgcaggat 420
gacatccggc tggcagccca gctggaggca ccccgccctc cccggctccg ctacctgctg 480
gtagtttcta cacgagaagg agaaggctcg agccaggatg agacgggtcct cctgggcgtg 540
gatttcctcg acagcagctc ccccagctgc accctggggc tggctctgcc cctctggagt 600
gacacccagg tgtacttaga tggagacggg ggcttcagcg tgacgtctgg tgggcaaagc 660
cggatcttca agcccatctc catccagacc atgtgggcca cactccaggg attgcaccaa 720
gcatgtgagg cagctctagg cagcggcctt gtaccgggtg gcagtgcctt cacctggggc 780
agccactacc aggagagact gaactccgaa cagagctgcc tcaatgagtg gacggctatg 840
gccgacctgg agtctctgcg gcctcccagc gccgagcctg gcgggtcctc agaacaggag 900
cagatggagc aggcgatccg tgcctgagctg tggaaagtgt tggatgtcag tgacctggag 960
agtgtcactt ccaaagagat ccgccaggct ctggagctgc gcctggggct cccctccag 1020
cagtaccgtg acttcatcga caaccagatg ctgctgctgg tggcacagcg ggaccgagcc 1080
tcccgcatct tccccacact ctacctgggc tcagagtggg acgcagcaaa cctggaggag 1140
ctgcagagga acagggtcac ccacatcttg aacatggccc gggagattga caacttctac 1200
cctgagcgct tcacctacca caatgtgcgc ctctgggatg aggagtccgc ccagctgctg 1260
ccgcaactga aggagacgca ccgcttcatt gaggtgcaa gagcacaggg caccacagt 1320
ctggtccact gcaagatggg cgtcagccgc tcagcggcca cagtgtggc ctatgccatg 1380
aagcagtacg aatgcagcct ggagcaggcc ctgcgccacg tgcaggagct ccggcccatc 1440
gcccgcacca accctggctt cctgcgccag ctgcagatct accagggcct cctgacggcc 1500
agaacctgag ggtggtgggg aggagaaggt tgtaggctag gaagagagcc aggcagcccc 1560
gaaagaagag cctggggcca ggccacgtat aaacctccga ggggtcatga ggtccatcag 1620
tcttctggag cctccttgag agctggagag cacctcagag accagtgaac tgccagaggt 1680
cttctcttcc cagcagctctt cacatgaaga gcctctgcag cccttccac agcttgcaag 1740
gaccaagggg ggccagcagg tggacagggg gcctcagcct gccctgaagt cccgccagtc 1800
agtgtgtacc ctccagggca gtgccgtggt ggccaaccgg acccaggcct tccaggagca 1860
ggagcagggg caggggagag ggcagggaga gccctgcatt tctctacgc ccaggttccg 1920
gaaggtggtg agacaggcca gcgtgcatga cagtggagag gagggcgagg cctgagccct 1980
cacacatgcc cagctcccc tgacactgaa gaggatccac aactccttgg agaaacaccc 2040
tcacgtctgt tgcgcacac attcctctca gctccgcccc ataccctgca ctacagcctc 2100
acctcccacc cctgtcacta cggcctcacc tcccaccctt gtcactacag cctcacctcc 2160
tacagcctta agtcccaggc ccatgtctgc ctgtccaagg gctcaagact ttctaactgg 2220
gatgtggtag agggactgaa ggtacctttg ggggcaacag caccctagtt tcattctcaa 2280
ctctagccct gcacactcac ctgtggcacg gaatgaaaac agagcttccc gtgcaaaaag 2340
ggtcacgcct cccacccccg cccctccctt gcacctcctg tctctccca gttcattcct 2400
ggaaccagcc aggcaggca accagtggcc cccaaaggca ggcaggatcc tcaggccccca 2460
gccgcgggag gctggaaggg ctggcagatc gcttccctca tccacctcca ccggtccagg 2520
tctttgctgc tgtcccaga cctcctgtga caccagcca gatcacaggg caccaggcca 2580
gagatagtct tctttttgtc ctttctggcc tctggctagt cagtttttca tagccttaca 2640
gtatctggct ttgtactgag aaataaaaca cattttcata aaaaaaaaaa aaaaaaaaaa 2700
aaaa 2704
```

<210> 8

<211> 312

<212> PRT

<213> Human

<400> 8

Met Ala Leu Val Thr Val Ser Arg Ser Pro Pro Gly Ser Gly Ala Ser



1				5					10					15			
Thr	Pro	Val	Gly	Pro	Trp	Asp	Gln	Ala	Val	Gln	Arg	Arg	Ser	Arg	Leu		
			20					25					30				
Gln	Arg	Arg	Gln	Ser	Phe	Ala	Val	Leu	Arg	Gly	Ala	Val	Leu	Gly	Leu		
		35					40					45					
Gln	Asp	Gly	Gly	Asp	Asn	Asp	Asp	Ala	Ala	Glu	Ala	Ser	Ser	Glu	Pro		
	50				55						60						
Thr	Glu	Lys	Ala	Pro	Ser	Glu	Glu	Glu	Leu	His	Gly	Asp	Gln	Thr	Asp		
65					70					75					80		
Phe	Gly	Gln	Gly	Ser	Gln	Ser	Pro	Gln	Lys	Gln	Glu	Glu	Gln	Arg	Gln		
				85					90					95			
His	Leu	His	Leu	Met	Val	Gln	Leu	Leu	Arg	Pro	Gln	Asp	Asp	Ile	Arg		
			100					105					110				
Leu	Ala	Ala	Gln	Leu	Glu	Ala	Pro	Arg	Pro	Pro	Arg	Leu	Arg	Tyr	Leu		
		115					120					125					
Leu	Val	Val	Ser	Thr	Arg	Glu	Gly	Glu	Gly	Leu	Ser	Gln	Asp	Glu	Thr		
	130					135					140						
Val	Leu	Leu	Gly	Val	Asp	Phe	Pro	Asp	Ser	Ser	Ser	Pro	Ser	Cys	Thr		
145					150					155					160		
Leu	Gly	Leu	Val	Leu	Pro	Leu	Trp	Ser	Asp	Thr	Gln	Val	Tyr	Leu	Asp		
				165				170						175			
Gly	Asp	Gly	Gly	Phe	Ser	Val	Thr	Ser	Gly	Gly	Gln	Ser	Arg	Ile	Phe		
			180					185					190				
Lys	Pro	Ile	Ser	Ile	Gln	Thr	Met	Trp	Ala	Thr	Leu	Gln	Val	Leu	His		
	195					200						205					
Gln	Ala	Cys	Glu	Ala	Ala	Leu	Gly	Ser	Gly	Leu	Val	Pro	Gly	Gly	Ser		
	210				215						220						
Ala	Leu	Thr	Trp	Ala	Ser	His	Tyr	Gln	Glu	Arg	Leu	Asn	Ser	Glu	Gln		
225					230					235					240		
Ser	Cys	Leu	Asn	Glu	Trp	Thr	Ala	Met	Ala	Asp	Leu	Glu	Ser	Leu	Arg		
			245						250					255			
Pro	Pro	Ser	Ala	Glu	Pro	Gly	Gly	Ser	Ser	Glu	Gln	Glu	Gln	Met	Glu		
			260					265						270			
Gln	Ala	Ile	Arg	Ala	Glu	Leu	Trp	Lys	Val	Leu	Glu	Leu	Glu	Ser	Thr		
		275					280					285					
Ser	Glu	Thr	Ser	Asp	Met	Pro	Glu	Val	Phe	Ser	Ser	His	Glu	Ser	Ser		
	290				295						300						
His	Glu	Glu	Pro	Leu	Gln	Pro	Phe										
305					310												

<210> 9

<211> 524

<212> PRT

<213> *Drosophila melanogaster*

<400> 9

Met	Ala	Leu	Val	Thr	Val	Gln	Arg	Ser	Pro	Ser	Val	Ala	Gly	Ser	Cys		
1				5					10				15				
Ser	Asn	Ser	Asp	Gly	Glu	Ser	Glu	Asp	Asp	Glu	Gly	Asn	Ser	Lys	Gly		
		20						25				30					
Asn	Asp	Arg	Ser	Glu	Cys	Phe	Phe	Ala	Gly	Lys	Gly	Thr	Ala	Leu	Val		
	35					40						45					
Leu	Ala	Leu	Lys	Asp	Ile	Pro	Pro	Leu	Thr	Gln	Ser	Glu	Arg	Arg	Leu		
	50				55					60							
Ser	Thr	Asp	Ser	Thr	Arg	Ser	Ser	Asn	Ser	Thr	Gln	Ser	Asn	Asn	Ser		
65					70					75					80		

Asp	Ile	Gln	Leu	His	Leu	Gln	Ser	Met	Phe	Tyr	Leu	Leu	Gln	Arg	Glu	
				85					90					95		
Asp	Thr	Leu	Lys	Met	Ala	Val	Lys	Leu	Glu	Ser	Gln	Arg	Ser	Asn	Arg	
			100					105					110			
Thr	Arg	Tyr	Leu	Val	Ile	Ala	Ser	Arg	Ser	Cys	Cys	Arg	Ser	Gly	Thr	
		115					120					125				
Ser	Asp	Arg	Arg	Arg	His	Arg	Ile	Met	Arg	His	His	Ser	Val	Lys	Val	
	130					135					140					
Gly	Gly	Ser	Ala	Gly	Thr	Lys	Ser	Ser	Thr	Ser	Pro	Ala	Val	Pro	Thr	
145					150					155				160		
Gln	Arg	Gln	Leu	Ser	Val	Glu	Gln	Thr	Ala	Thr	Glu	Ala	Ser	Ser	Lys	
			165						170				175			
Cys	Asp	Lys	Thr	Ala	Asp	Lys	Glu	Asn	Ala	Thr	Ala	Ala	Gly	Asp	Asn	
			180					185					190			
Lys	Asn	Thr	Ser	Gly	Met	Glu	Glu	Ser	Cys	Leu	Leu	Gly	Ile	Asp	Cys	
		195					200					205				
Asn	Glu	Arg	Thr	Thr	Ile	Gly	Leu	Val	Val	Pro	Ile	Leu	Ala	Asp	Thr	
	210					215					220					
Thr	Ile	His	Leu	Asp	Gly	Asp	Gly	Gly	Phe	Ser	Val	Lys	Val	Tyr	Glu	
225					230					235				240		
Lys	Thr	His	Ile	Phe	Lys	Pro	Val	Ser	Val	Gln	Ala	Met	Trp	Ser	Ala	
				245					250					255		
Leu	Gln	Thr	Leu	His	Lys	Val	Ser	Lys	Lys	Ala	Arg	Glu	Asn	Asn	Phe	
			260					265					270			
Tyr	Ala	Ser	Gly	Pro	Ser	His	Asp	Trp	Leu	Ser	Ser	Tyr	Glu	Arg	Arg	
	275						280					285				
Ile	Glu	Ser	Asp	Gln	Ser	Cys	Leu	Asn	Glu	Trp	Asn	Ala	Met	Asp	Ala	
	290					295					300					
Leu	Glu	Ser	Arg	Arg	Pro	Pro	Ser	Pro	Asp	Ala	Ile	Arg	Asn	Lys	Pro	
305					310					315				320		
Pro	Glu	Lys	Glu	Glu	Thr	Glu	Ser	Val	Ile	Lys	Met	Lys	Leu	Lys	Ala	
				325					330					335		
Ile	Met	Met	Ser	Val	Asp	Leu	Asp	Glu	Val	Thr	Ser	Lys	Tyr	Ile	Arg	
			340					345					350			
Gly	Arg	Leu	Glu	Glu	Ile	Leu	Asp	Met	Asp	Leu	Gly	Glu	Tyr	Lys	Ser	
		355					360					365				
Phe	Ile	Asp	Ala	Glu	Met	Leu	Val	Ile	Leu	Gly	Gln	Met	Asp	Ala	Pro	
	370					375					380					
Thr	Lys	Ile	Phe	Glu	His	Val	Tyr	Leu	Gly	Ser	Glu	Trp	Asn	Ala	Ser	
385					390					395				400		
Asn	Leu	Glu	Glu	Leu	Gln	Lys	Asn	Gly	Val	Arg	His	Ile	Leu	Asn	Val	
			405						410					415		
Thr	Arg	Glu	Ile	Asp	Asn	Phe	Phe	Pro	Gly	Thr	Phe	Glu	Tyr	Phe	Asn	
		420						425					430			
Val	Arg	Val	Tyr	Asp	Asp	Glu	Lys	Thr	Asn	Leu	Leu	Lys	Tyr	Trp	Asp	
		435					440					445				
Asp	Thr	Phe	Arg	Tyr	Ile	Thr	Arg	Ala	Lys	Ala	Glu	Gly	Ser	Lys	Val	
	450					455					460					
Leu	Val	His	Cys	Lys	Met	Gly	Val	Ser	Arg	Ser	Ala	Ser	Val	Val	Ile	
465					470					475				480		
Ala	Tyr	Ala	Met	Lys	Ala	Tyr	Gln	Trp	Glu	Phe	Gln	Gln	Ala	Leu	Glu	
				485					490					495		
His	Val	Lys	Lys	Arg	Arg	Ser	Cys	Ile	Lys	Pro	Asn	Lys	Asn	Phe	Leu	
		500						505					510			
Asn	Gln	Leu	Glu	Thr	Tyr	Ser	Gly	Met	Leu	Asp	Ala					
		515					520									

<210> 10  
 <211> 111  
 <212> PRT  
 <213> Human

<400> 10

Met	Ala	Arg	Glu	Ile	Asp	Asn	Phe	Tyr	Pro	Glu	Arg	Phe	Thr	Tyr	His
1				5					10					15	
Asn	Val	Arg	Leu	Trp	Asp	Glu	Glu	Ser	Ala	Gln	Leu	Leu	Pro	His	Trp
			20					25					30		
Lys	Glu	Thr	His	Arg	Phe	Ile	Glu	Ala	Ala	Arg	Ala	Gln	Gly	Thr	His
		35					40					45			
Val	Leu	Val	His	Cys	Lys	Met	Gly	Val	Ser	Arg	Ser	Ala	Ala	Thr	Val
	50					55					60				
Leu	Ala	Tyr	Ala	Met	Lys	Gln	Tyr	Glu	Cys	Ser	Leu	Glu	Gln	Ala	Leu
65					70				75						80
Arg	His	Val	Gln	Glu	Leu	Arg	Pro	Ile	Ala	Arg	Pro	Asn	Pro	Gly	Phe
			85						90					95	
Leu	Arg	Gln	Leu	Gln	Ile	Tyr	Gln	Gly	Ile	Leu	Thr	Ala	Arg	Thr	
			100					105						110	